

Appendix I: Alignment of instant SEQ ID NO: 1 and Q9H4I2, publicly available June 2002

BLASTP 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

RID: KMB3KFZ911R

Query= SID_1
Length=956

Sequences producing significant alignments:		Score (Bits)	E Value
lcl 22739	TrEMBL Q9H4I2 Release 21 01-JUN-2002	1989	0.0

ALIGNMENTS

>lcl|22739 TrEMBL|Q9H4I2|Release 21|01-JUN-2002
Length=956

Score = 1989 bits (5152), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 956/956 (100%), Positives = 956/956 (100%), Gaps = 0/956 (0%)

Query 1	MASKRKSTTPCMIPVKTVVLQDASMEAQPAETLPEGPQQDLPPEASAASSEAAQNPSSSTD	60
Sbjct 1	MASKRKSTTPCMIPVKTVVLQDASMEAQPAETLPEGPQQDLPPEASAASSEAAQNPSSSTD	60
Query 61	GSTLANGHRSTLDGYLYSCKYCDFRSHDMTQFVGHMNSEHTDFNKDPTFVCSGCSFLAKT	120
Sbjct 61	GSTLANGHRSTLDGYLYSCKYCDFRSHDMTQFVGHMNSEHTDFNKDPTFVCSGCSFLAKT	120
Query 121	PEGLSLHNATCHSGEASFVWNVAKPDNHHVVVEQSipeSTSTPDLAGEPSEAEGADGQAEII	180
Sbjct 121	PEGLSLHNATCHSGEASFVWNVAKPDNHHVVVEQSipeSTSTPDLAGEPSEAEGADGQAEII	180
Query 181	ITKTPIMKIMKGKAEAKKIHTLKENVPSQPVGAEALPKLSTGEMEVREGDHSFINGAVPVS	240
Sbjct 181	ITKTPIMKIMKGKAEAKKIHTLKENVPSQPVGAEALPKLSTGEMEVREGDHSFINGAVPVS	240
Query 241	QASASSAKNPHANGPLIGTPVLPAGIAQFLSLQQQPPVHAQHHVHQPLPTAKALPKVM	300
Sbjct 241	QASASSAKNPHANGPLIGTPVLPAGIAQFLSLQQQPPVHAQHHVHQPLPTAKALPKVM	300
Query 301	IPLSSIPTYNAAMDSNSFLKNSFHKFPTKAELCYLTVVTKYPEEQLKIWFTAQRALKQG	360
Sbjct 301	IPLSSIPTYNAAMDSNSFLKNSFHKFPTKAELCYLTVVTKYPEEQLKIWFTAQRALKQG	360
Query 361	ISWSPEEIEDARKKMFNTVIQSVPOPTITVLNTPLVASAGNVQHLIQAAALPGHVVGQPEG	420

Sbjct	361	ISWSPEEIEDARKKMFNTVIQSVQOPTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEG ISWSPEEIEDARKKMFNTVIQSVQOPTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEG	420
Query	421	TGGGLLVTQPLMANGLQATSSPLPLTVTSVPKQPGVAPINTVCSNTTSAVKVVNAAQSLL TGGGLLVTQPLMANGLQATSSPLPLTVTSVPKQPGVAPINTVCSNTTSAVKVVNAAQSLL	480
Sbjct	421	TGGGLLVTQPLMANGLQATSSPLPLTVTSVPKQPGVAPINTVCSNTTSAVKVVNAAQSLL	480
Query	481	TACPSITSQAFLDASIYKNKKSHEQSALKGSFCRNFQFPQSEVEHLTKVTGLSTREVRK TACPSITSQAFLDASIYKNKKSHEQSALKGSFCRNFQFPQSEVEHLTKVTGLSTREVRK	540
Sbjct	481	TACPSITSQAFLDASIYKNKKSHEQSALKGSFCRNFQFPQSEVEHLTKVTGLSTREVRK	540
Query	541	WFSDRRYHCRNLKGSRAMIPGDHSSIIIDSVPFSPSSKVPEVTCIPTTATLATHPSA WFSDRRYHCRNLKGSRAMIPGDHSSIIIDSVPFSPSSKVPEVTCIPTTATLATHPSA	600
Sbjct	541	WFSDRRYHCRNLKGSRAMIPGDHSSIIIDSVPFSPSSKVPEVTCIPTTATLATHPSA	600
Query	601	KRQSWHQTPDFPTKYKERAPEQLRALESSFAQNPLPLDEELDRLRSETKMTRREIDSWF KRQSWHQTPDFPTKYKERAPEQLRALESSFAQNPLPLDEELDRLRSETKMTRREIDSWF	660
Sbjct	601	KRQSWHQTPDFPTKYKERAPEQLRALESSFAQNPLPLDEELDRLRSETKMTRREIDSWF	660
Query	661	SERRKKVNAEETKKAEEENASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAER SERRKKVNAEETKKAEEENASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAER	720
Sbjct	661	SERRKKVNAEETKKAEEENASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAER	720
Query	721	KVSPIKINLKNLRVTEANGRNEIPGLGACDPEDDESNKLAEQLPGKVSCKKTAQQRHLLR KVSPIKINLKNLRVTEANGRNEIPGLGACDPEDDESNKLAEQLPGKVSCKKTAQQRHLLR	780
Sbjct	721	KVSPIKINLKNLRVTEANGRNEIPGLGACDPEDDESNKLAEQLPGKVSCKKTAQQRHLLR	780
Query	781	QLFVQTQWPSNQDYDSIMAQTGLPPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLL QLFVQTQWPSNQDYDSIMAQTGLPPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLL	840
Sbjct	781	QLFVQTQWPSNQDYDSIMAQTGLPPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLL	840
Query	841	VIAPGNRELLQDYYMTHKMLYEEIDLQNLCDKTQMSSQQVKQWFAEKMGEEETRAVADTGSE VIAPGNRELLQDYYMTHKMLYEEIDLQNLCDKTQMSSQQVKQWFAEKMGEEETRAVADTGSE	900
Sbjct	841	VIAPGNRELLQDYYMTHKMLYEEIDLQNLCDKTQMSSQQVKQWFAEKMGEEETRAVADTGSE	900
Query	901	DQGPGTGELTAVHKGMGDTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD DQGPGTGELTAVHKGMGDTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD	956
Sbjct	901	DQGPGTGELTAVHKGMGDTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD	956